(FILE 'HOME' ENTERED AT 12:55:07 ON 13 AUG 2002)

```
      FILE 'MEDLINE, CAPLUS, EMBASE, BIOSIS' ENTERED AT 12:55:30 ON 13 AUG 2002
L1              7 S PRO269
L2              4 DUP REM L1 (3 DUPLICATES REMOVED)
L3              0 S VP15_1
L4           7499 S THROMBOMODULIN
L5           2089 S L4 AND (HOMOLOG? OR GENE OR STRUCTURE)
L6            999 S L5 AND PY<1998
L7              1 S L6 AND HYPERTROPHY
L8          25167 S (HEART OR CARDIAC) (1W) HYPERTROPHY
L9              1 S L8 AND L4
L10          6137 S L8 AND (MODEL OR PHENYLEPHRIN)
L11           891 S L10 AND MYOCYTES
L12            88 S L11 AND (INHIBIT OR BLOCK OR REDUCE OR PROTECT)
L13            58 DUP REM L12 (30 DUPLICATES REMOVED)
L14             0 S L10 AND UNPREDICTABLE
L15           131 S L10 AND ANTIBODY
L16            86 DUP REM L15 (45 DUPLICATES REMOVED)
L17            48 S L16 AND PY<1998
```

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Notice - Please read carefully prior to linking to any third-party site.

GeneCard for gene THBD   Approved UCL/HGNC/HUGO Human Gene Nomenclature database symbol
THBD (thrombomodulin)

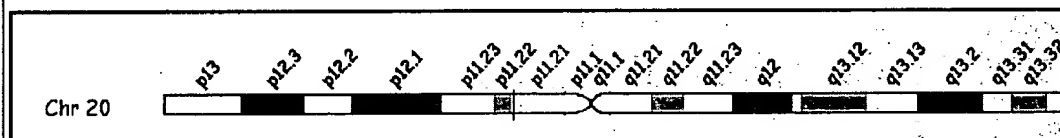|	
Aliases and Additional Descriptions (According to GDB, HUGO, and/or SWISS-PROT)	• THRM • **thrombomodulin** • **Thrombomodulin** precursor (Fetomodulin) (TM) (CD141 antigen).
Chromosomal Location (According to LocusLink and/or UDB and/or HUGO, Genomic Views According to UCSC and Ensembl)	*Chromosome:* **20** *LocusLink cytogenetic band:* **20p12-cen** *Ensembl cytogenetic band:* *Unified DataBase coordinate (from pter):* 24,473 mega bases *Genomic View:* UCSC Golden Path
Proteins (According to SWISS-PROT and/or MIPS)	TRBM_HUMAN **Size**: 575 amino acids; 60329 Da **Function: thrombomodulin is a specific endothelial cell receptor that forms a 1: 1 ST** CONVERSION OF PROTEIN C TO THE ACTIVATED PROTEIN C (PROTEIN CA). ONCE MECHANISM, FACTOR VA AND FACTOR VIIIA, AND THEREBY REDUCES THE AMOU **Subcellular location**: Type I membrane protein. **Tissue specificity**: ENDOTHELIAL CELLS ARE UNIQUE IN SYNTHESIZING **THROMB(** **Polymorphism**: VARIATIONS IN THBD ARE ASSOCIATED WITH AN INCREASED RISI **Similarity**: CONTAINS 6 EGF-LIKE DOMAINS. **3D structures**: PDB ids 1EGT **(3D)** 1FGD **(3D)** 1FGE **(3D)** 1TMR **(3D)** 1ZAQ **(3D)** : **MIPS Pedant Viewer**: 682 **REFSEQ proteins**: NP_000352.1

Pr tein D mains/Families (According to BLOCKS and/or InterPro)	**Blocks protein families:**
	
	    BL00615 C-type lectin domain proteins.
	
	    BL01187 Calcium-binding EGF-like domain proteins pattern proteins.
	
	    PR00907 Thrombomodulin signature
	
	InterPro D mains and Families:
	
	    IPR001304; Lectin_C
	    IPR001491; Thrmbomodulin

IPR000561; EGF-like
IPR001881; EGF_Ca
IPR000152; Asx_hydroxyl

Graphical View of Domain Structure for SP Entry P07204

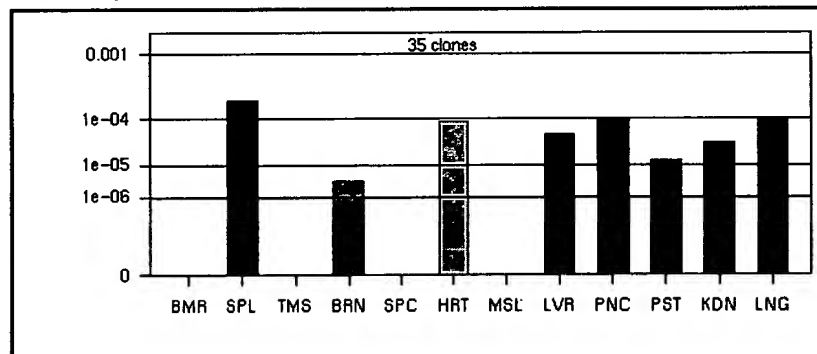|	
Sequences (GenBank/EMBL/DDBJ Accessions According to Unigene or GenBank, RefSeq According to LocusLink, Assembly According to MIPS and/or DOTS)	**REFSEQ mRNAs:** NM_000361.1 **Additional Gene/cDNA sequence:** D00210.1 J02973.1 M16552 M16552.1 X05495 X05495.1 **MIPS assembly:**H426S1 **DOTS assembly:** DT.416446 DT.92427530 DT.92427529 **Unigene Cluster for THBD:** (Build 151 Homo sapiens; May 27 2002) **thrombomodulin** Hs.2030 [show with all **ESTs**] **Unigene Representative Sequence:** NM_000361
Expression in Human Tissues (According to proprietary W.I.S DNA array results, UniGene and/or SOURCE)	**THBD expression in normal human tissues based on quantifying ESTs from various** SOURCE GeneReport for Unigene cluster Hs.2030

Homologues:

	gene	locus	description
Similar Genes in Other Organisms (According to MGD Jun 10 2002 , Stony Brook C.elegans-H.sapiens Alignment Database and/or euGenes)	mouse (MGD)	Thbd	2 (84.00 cM)	thrombomodulin
	fly (euGenes)	ple	3 65C3	catecholamine metabolism tyrosine 3-monooxygen:
	C. elegans (Stony Brook)	W07G4.4	--	description: ke58e03.y1 Dirofilaria immitis adult SL· immitis cDNA similar to SW:YH24_CAEEL Q27245 AMINOPEPTIDASE W07G4.4 IN CHROMOSOME

Variants: SWISS-PROT: TRBM_HUMAN

NCBI SNPs: 10/18 selected, not withdrawn, single nucleotide mutations are shown here.
Click here to see all of them

				Genomic Data				
SNP ID	C ntig Accession	P siti n in C ntig	Strand	5' Flanking Sequenc *	3' Flanking Sequ
rs1042579	NT_011387.7	22966781	-	CCGACTCGGCCCTTG	CCGCCACATTGC
rs3176121	NT_011387.7	22966313	-	CTAACTGGCGAGGGG	TGATTAGAGGG/
rs3176122	NT_011387.7	22965974	-	GTAAACTATCTTGGT	AATTTTTTTTTC
rs3176123	NT_011387.7	22965470	-	GGTTGCTCTAGATTG	GAGAAGAGACA/
rs3176124	NT_011387.7	22965002	-	TCAGGCCCTTATTTT	AAGAAACTGAGC
rs3176133	NT_011387.7	22966384	-	CACCTTAGCTGGCAT	ACAGCTGGAGA/
rs3176134	NT_011387.7	22966194	-	CAGGTCCTCACTACC	GGCGCAGGAGG(
rs1042580	NT_011387.7	22965678	-	TGAGATGTAAAAGGT	TTAAATTGATGT
rs3176117	NT_011387.7	22969818	-	GACGCCATACTCTCT	TTCTTGTTTAAA
rs3176119	NT_011387.7	22969167	-	CAATTCACCTGCCAC	GCCTCTGAGCC(

SNPs/Variants
(According to the NCBI SNP Database and to SWISS-PROT)

* *Lower case letters indicate repetitive or low-complexity sequence*

All NCBI SNPs in THBD

Disorders & Mutations
(in which this Gene is Involved, According to OMIM, SWISS-PROT, Genatlas, GeneClinics, HGMD, BCGD, and/or TGDB.)

OMIM ID: 188040

search databases for MIM named disorders:
- Thrombophilia due to **thrombomodulin** defect
- {Myocardial

SWISS-PROT: TRBM_HUMAN

- **Disease:** DEFECTS IN THBD COULD BE THE CAUSE OF INHERITED TED, ALSO HAEMOPOIETIC SYSTEM WHICH CREATES A TENDENCY TO THE OCCURREN CARDIOVASCULAR DISORDERS.

Genatlas disease: THBD

- thrombosis,recurrent

Human Gene Mutation Database entry for THBD

Medical News
(Possibly Related Articles in Doctor's Guide)

--

Research Articles
(in PubMed)

- Structure and expression of human **thrombomodulin**, a thrombin receptor on endotl

| Search PubMed for THBD | to find abstracts of **research articles** containing

THBD in Other Genome Wide Resources:
(According to GDB, LocusLink, euGenes, Ensembl and/or GeneLynx)

GDB: 119613   LocusLink: 7056   euGenes: HUgn7056   Ensembl: ENSG0000010

THBD in G neral Databases, Limited Scope
(According to HUGE)

--

THBD in Specialized Databases (According to <u>ATLAS</u>, <u>GENATLAS</u>, <u>HORDE</u>, <u>IMGT</u>, <u>MTDB</u> and/or <u>SWISS-PROT</u>)	*name* <u>**Genatlas**</u> biochemistry entry for THBD: thrombomodulin coagulation factor complexing w mutations in the promoter region putatively associated with a risk for arterial thrombosis a PROW -CD guide CD141 entry.
Services (According to <u>RZPD</u>)	<u>Search RZPD for clones of THBD</u> Clone collection at the German Human Genome Proje

Back (to Search Results)	- **More** like this

Search the web for THBD	- search millions of **Web pages** with **Excite** to find other web sites related

<u>GeneCards **Homepage**</u> - How to **Search** or **Cite** this Database - Last **Update**: 20 Jun 2002

S arch GeneCards for [   ] [Go]

<u>Display the GeneCard of a random gene</u>
<u>Display the GeneCard of a random HUGO-approved gene</u>

<u>The GeneCards **idea**</u> in brief: **Mining** the Internet for biomedical knowledge and **guiding** the user to it.

PR00907: THRMBOMODULN

Thrombomodulin signature

- ○ Introduction
- ○ Block number PR00907A
- ○ Block number PR00907B
- ○ Block number PR00907C
- ○ Block number PR00907D
- ○ Block number PR00907E
- ○ Block number PR00907F
- ○ Block number PR00907G
- ○ Block number PR00907H
- ○ Block number PR00907I

- ○ PRINTS Entry PR00907 (source of blocks)

- ○ Block Map [About Maps]

- ○ Logos.[About Logos]
  Select display format: [GIF] [PDF] [Postscript]

- ○ Tree from blocks alignment. [About Trees] [About ProWeb TreeViewer]
  [Data] [ProWeb TreeViewer] [XBitmap] [GIF] [PDF] [Postscript] [Newick]

- ○ PDB entries

- ○ Search blocks vs other databases:
  - ■ COBBLER sequence and BLAST searches [About COBBLER]
  - ■ MAST Search of all blocks vs a sequence database [About MAST]
  - ■ LAMA search of all blocks vs a blocks database [About LAMA]

- ○ CODEHOP to design PCR primers from blocks [About CODEHOP]

- ○ SIFT to predict amino acid substitutions in blocks [About SIFT]

- ○ Additional Links

```
        Calibrated with position-specific scoring matrices made with pseudo-counts,
        JG Henikoff & S Henikoff (1996), CABIOS 12(2):135-143.
        =======================================================================
```

[Return to top]

Block PR00907A

```
ID    THRMBOMODULN; BLOCK
AC    PR00907A; distance from previous block=(232,233)
DE    Thrombomodulin signature
BL    adapted;    width=20; seqs=3; 99.5%=823; strength=1362
O35370                  ( 232) GHWTREVTGAWNCSVENGGC 100
TRBM MOUSE|P15306       ( 232) GHWAWEATGAWNCSVENGGC  96
TRBM HUMAN|P07204       ( 233) GHWAREAPGAWDCSVENGGC 100
//
```

[Return to top]

Block PR00907B

```
ID    THRMBOMODULN; BLOCK
AC    PR00907B; distance from previous block=(-1,0)
DE    Thrombomodulin signature
BL    adapted;    width=17; seqs=3; 99.5%=734; strength=1262
O35370                  ( 251) CEYMCNRSANGPRCVCP  84
TRBM MOUSE|P15306       ( 251) CEYLCNRSTNEPRCLCP  84
TRBM HUMAN|P07204       ( 252) CEHACNAIPGAPRCQCP 100
//
```

[Return to top]

Block PR00907C

```
ID    THRMBOMODULN; BLOCK
AC    PR00907C; distance from previous block=(4,4)
DE    Thrombomodulin signature
BL    adapted;    width=24; seqs=3; 99.5%=941; strength=1371
O35370                  ( 272) LQADGRSCAKPVAQLCNELCQHFC  94
TRBM MOUSE|P15306       ( 272) LQADGRSCARPVVQSCNELCEHFC  88
TRBM HUMAN|P07204       ( 273) LQADGRSCTASATQSCNDLCEHFC 100
//
```

[Return to top]

Block PR00907D

```
ID    THRMBOMODULN; BLOCK
AC    PR00907D; distance from previous block=(48,48)
DE    Thrombomodulin signature
BL    adapted;    width=26; seqs=3; 99.5%=994; strength=1481
O35370                  ( 344) GGFECRCYDGYELVDGECVEQLDPCF  89
TRBM MOUSE|P15306       ( 344) GGFECFCYDGYELVDGECVELLDPCF  89
TRBM HUMAN|P07204       ( 345) GGFECHCYPNYDLVDGECVEPVDPCF 100
//
```

[Return to top]

Block PR00907E

```
ID    THRMBOMODULN; BLOCK
AC    PR00907E; distance from previous block=(3,3)
DE    Thrombomodulin signature
BL    adapted;    width=23; seqs=3; 99.5%=919; strength=1375
O35370                  ( 373) CEYQCQPVNSTHYNCICAEGFAP   91
TRBM MOUSE|P15306       ( 373) CEFQCQPVSPTDYRCICAPGFAP  100
TRBM HUMAN|P07204       ( 374) CEYQCQPLNQTSYLCVCAEGFAP   97
//
```

[Return to top]

Block PR00907F

```
ID    THRMBOMODULN; BLOCK
AC    PR00907F; distance from previous block=(4,4)
DE    Thrombomodulin signature
BL    adapted;    width=19; seqs=3; 99.5%=782; strength=1396
O35370                  ( 400) PDRCEMFCNETSCPADCDP   93
TRBM MOUSE|P15306       ( 400) PHKCEMFCNETSCPADCDP   93
TRBM HUMAN|P07204       ( 401) PHRCQMFCNQTACPADCDP  100
//
```

[Return to top]

Block PR00907G

```
ID    THRMBOMODULN; BLOCK
AC    PR00907G; distance from previous block=(35,35)
DE    Thrombomodulin signature
BL    adapted;    width=27; seqs=3; 99.5%=1038; strength=1431
O35370                  ( 454) CRNLPGSYECICGPDTALAGQISKDCD   80
TRBM MOUSE|P15306       ( 454) CRNFPGSYECICGPDTALAGQISKDCD   83
TRBM HUMAN|P07204       ( 455) CHNLPGTFECICGPDSALARHIGTDCD  100
//
```

[Return to top]

Block PR00907H

```
ID    THRMBOMODULN; BLOCK
AC    PR00907H; distance from previous block=(32,35)
DE    Thrombomodulin signature
BL    adapted;    width=25; seqs=3; 99.5%=918; strength=1397
O35370                  ( 516) HSGVLIGISIASLSLVVALLALLCH   94
TRBM MOUSE|P15306       ( 516) HSGVLIGISIASLSLVVALLALLCH   94
TRBM HUMAN|P07204       ( 514) HSGLLIGISIASLCLVVALLALLCH  100
//
```

[Return to top]

Block PR00907I

```
ID    THRMBOMODULN; BLOCK
AC    PR00907I; distance from previous block=(8,8)
DE    Thrombomodulin signature
BL    adapted;    width=25; seqs=3; 99.5%=931; strength=1340
O35370                  ( 549) RAELEYKCTSSAKEVVLQHVRTDRT   86
TRBM MOUSE|P15306       ( 549) RAELEYKCASSAKEVVLQHVRTDRT   84
TRBM HUMAN|P07204       ( 547) RAKMEYKCAAPSKEVVLQHVRTERT  100
```

//

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COBBLER sequence (region containing Blocks only)

To do a BLAST search, copy the cobbler sequence below then click on a BLAST link

[Blast Search] [Gap-Blast Search] [PSI-Blast Search]

COBBLER sequence:
>PR00907 O35370|O35370 from 222 to 577 with embedded consensus blocks
vcralpgtseGHWAREATGAWNCSVENGGCCEYMCNRSPNGPRCLCPggdlLQADGRSCAKPVTQSCNELCEHFCnnsdv
pgsyscmcetgyqlaadghrcedvddckqgpnpcpqlcsntegGGFECHCYDGYELVDGECVEPLDPCFskcCEYQCQPV
NPTHYRCICAEGFAPlddpPHRCEMFCNETSCPADCDPspsfcqcpegfildegsictdidecsqgecltnecCRNLPGS
YECICGPDTALAGQISKDCDipvledsedggsgehpssnptvvsstvppsarpmhHSGVLIGISIASLCLVVALLALLCH
rkkqgtarRAELEYKCASSAKEVVLQHVRTDRTqkf

[Return to top]

Additional Links (separate browser window)

InterPro IPR001491
PROSITE PS00022
MetaFam PR00907

[Blocks home]

73136

From:	Roark, Jessica
Sent:	Tuesday, August 13, 2002 9:19 AM
T :	Delaval, Jan
Subject:	09/902,713

Jan,

Please search, including pending, the following from 09/902,713:

SEQ ID NO:96
SEQ ID NO:96 oligo.

Results on paper please.

Thanks!

Jessica H. Roark
CM1 8A03
Mailbox 9E12
Art Unit 1644
703 605-1209

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov